

From: STIC-ILL
Sent: Wednesday, December 26, 2001 6:14 AM
To: STIC-Biotech/ChemLib
Subject: RE: 09/497967

-----Original Message-----

From: Fields, Iesha
Sent: Monday, December 24, 2001 11:02 AM
T : STIC-ILL
Subject: 09/497967

Please do a sequence search and interference search on SEQ ID NO:7 for Application 09/497967.

Thank You

Iesha Fields
Art Unit 1645
Mailbox 8E-12
Room 8A-13
605-1208

Point of Contact:
Toby Port
Technical Info. Specialist
CM1 ~~TEOT~~ TEL: 308-3534
12C14

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 12/26
Date Completed: 12/26
Searcher Prep/Review: 10
Clerical: _____
Online time: 10

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: 1 _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST(where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: cg _____
WWW/Internet: _____
Other (specify): _____

REC'D BY: _____
(STM)
12/26/01
RECEIVED

1000
1000
1000

C; Species: Giardia lamblia	NC- NLEAGKSQCLKCPVSKTTPAHA -PGNTATQATQCLTTPCAGTVLDDGTTSTNFVASAT	353
C; Date: 05-Dec-1998 #sequence-revision 05-Dec-1998 #text_change 01-Dec-2000		
C; Accession: A42125; B42125; S00530; S48056		
R; Adam, R.D.; Yang, Y.M.; Nash, T.E.		
Mol. Cell. Biol. 12, 1194-1201, 1992		
A; Title: The cysteine-rich protein gene family of Giardia lamblia: loss of the CRP170		
A; Reference number: A42125; MUID: 92186850		
A; Accession: A42125		
A; Molecule type: DNA		
A; Residues: 1-98 <ADA1>		
A; Cross references: GB: M83937; NID: 9159124		
A; Experimental source: trophozoite		
A; Note: sequence extracted from NCBI backbone (NCBIN: 88021, NCBIP: 88427); this ORF is		
A; Note: the authors report but do not show 19 tandem repeats of the sequence of resid		
A; Accession: B42125		
A; Molecule type: DNA		
A; Residues: 1-69-1766 <ADA2>		
A; Cross references: GB: M83933; NID: 9159122		
A; Note: sequence extracted from NCBI backbone (NCBIN: 88024, NCBIP: 88431); this ORF is		
R; Adam, R.D.; Aggarwal, A.; Lal, A.A.; de la Cruz, V.F.; McCutchan, T.; Nash, T.E.		
J. Exp. Med. 167, 109-118, 1988		
A; Title: Antigenic variation of a cysteine-rich protein in Giardia lamblia.		
A; Reference number: S00530; MUID: 88089405		
A; Accession: S00530		
A; Molecule type: DNA		
A; Residues: 1154-1409, 'A', 1411-1420, 'K', 1422-1425, 'R', 1427-1481 <ADA3>		
A; Cross references: EMBL: X67641; NID: 99355; PID: 9929603		
R; Yang, Y.; Adam, R.D.		
Nucleic Acids Res. 22, 2102-2108, 1994		
A; Title: Allele-specific expression of a variant-specific surface protein (VSP) of Gi		
A; Reference number: S48056; MUID: 94301794		
A; Accession: S48056		
A; Molecule type: DNA		
A; Residues: 1-56 <YAN>		
A; Cross references: EMBL: L25059		
A; Experimental source: trophozoites WBA6		
A; Note: the source is designated as Giardia intestinalis		
C; Comment: This translation was produced by PIR staff from information provided by th		
C; Genetics:		
A; Gene: VSPA6		
C; Keywords: surface antigen; tandem repeat		
Query Match 10.1%; Score 256.5; DB 2; Length 677;		
Best Local Similarity 25.0%; Pred. No. 1, 8e-09;		
Matches 121; Conservative 39; Mismatches 163; Indels 161; Gaps 32;		
Y 17 QIKSANCPVGTEWTNTAGQYDGLTPANCYNCOKNFFYNNAAAFV---PGASTCTP--- 68		
b 50 QAAAAGC----TKRGAALDKM1-ATCEPKCGDGYFLPMGGCYKTTDGPGESEICTKAEG 103		
Y 69 -CPOKKDA GAQPPIPATTNLVHQCNVCPGATTAAGTADYAAITTECVNCINFINEN 126		
b 104 LCTECKTANGLFKAAPTAPEKKGSEC-TLCG---SDINGDTGTG-VANCAQC-----T 150		
Y 127 APNFNAGASTCTACPVNRV-----GGALTAGNATIVAQCNVACPTGTALDDGV 176		
b 151 KSDSNKGAACTCATCAGYKDFQACSKCIGTCUTCTCCTSA---AQC-TSCPEG ----- 198		
Y 177 TDYVRSFTEVKCRLNFFYNGNNGTPFPKGSKCCTPCAIKPANVAQMTLGNDATIA 236		
b 199 -KYLKGDKSCVN-----ANGCTGNTYAAPESGKCLPCTNTIDA-----CTQ 238		
Y 237 CNVACPDTGTTSAAGYNNWVAQNTCTECPNPFNPNNTCLCPANKRDYABA 296		
b 239 CEV---DST-----TRKPKNCTNCQQMVKTAID---GTTTCV ----- 270		
Y 297 TAGGAATLAKQCNIACPDGTAIASGATNYVILQTECLNCAANFYEDGNNFOA -GSSRCK 354		
b 271 DANGCAT---SNV---DGSFLNDGS-----TRKCIILSD---DSELEANGTPGCK 313		
Y 355 AC PANKVQGAVATA-----GGATLILIQCALCPCAGTVLTDGTTSITYKQAASE 402		
b 314 TCCKN---GAKPTCSECLDGYYNSNGNGTIVTECA-CGANC-----ATCTQAGND 358		
Y 403 -CVKCAANFY---TUKQDTCVSCNK-----GIDTCVSCNK-----KLTSSEAEANIPESAKK 446		
b 359 KCTKCKPGFMKGNGPTECVAIDNAQGGIDGCAECTKESTGPLKCTKCKPNRKPAQISD 418		
Y 447 NIQC 450		
b 419 NYTC 422		
Y 285 PCPANKDYGAEATAGAATLAKQCNIACPDGTAIAS---GATNY----VILQTECLNC 335		
b 286 ACAGTADKCTKCDANGAAYPLKTNPSDPTGTCVSYAVDCQSGACYXTDDSVDAKECKRC 345		
Y 336 AANFYFDGNNFQASSRKACPAKNUVQGAVATAGGTATLIAQCALECPAGTFLV----- 388		

Db	346	-----NAPCTACAGTADKCTKCDANGAAYPLKKTNPSDPTGTCVSAVDCQG	391	
Qy	389	----TDGTTSTYKQ-----AASECVKCAAN-----	409	RESULT 5
Db	392	SAGYYTDDSVDAKECKCNAPCTACAGTADKCTKCDANGAAYPLKKTNPSDPTGTCVSA	451	A35502 major surface-labeled trophozoite antigen precursor - Giardia lamblia
Qy	410	-----FYTTKTDKVAGIDCTCTSNKKTSGAEANLPEASAKNIQCD 451		C;Species: Giardia lamblia
Db	452	VDCQGSAYYT---DDSVDAKECKCNAPCTACAGTADKCTKCD 493		C;Accession: A35502
RESULT 4				R;Gillin, F.D.; Harbold, P.; Harwood, J.; Aley, S.B.; Reiner, D.S.; McCaffery, M.; So Proc. Natl. Acad. Sci. U.S.A. 87, 4463-4467, 1990
A;Reference number: A48579; MUID:90280395				#sequence_revision 09-Nov-1990 #text_change 09-Sep-1997
A;Title: Isolation and expression of the gene for a major surface protein of Giardia trophozoite surface protein TSP11 - Giardia lamblia				A;Title: Isolation and expression of the gene for a major surface protein of Giardia trophozoite surface protein TSP11 - Giardia lamblia
C;Species: Giardia lamblia				A;Cross-references: GB:M33641; NID:9159131; PID:9159132
C;Accession: A48579				C;Keywords: surface antigen; transmembrane protein
A;Status: preliminary				
A;Molecule type: DNA				
A;Contents: Ad-1				
A;Accession: A48579				
A;Status: preliminary				
A;Molecule type: nucleic acid				
A;Cross-references: GB:W5814; NID:9159106; PID:9159107				
A;Title: A gene encoding a 69-kilodalton major surface protein of Giardia intestinalis				
A;Reference number: A48579; MUID:9241215				
A;Note: sequence extracted from NCBI backbone (NCBIN:130056, NCBIPI:130058)				
Query Match 9 3%; Score 236 5; DB 2; Length 667;				
Best Local Similarity 22.7%; Pred. No. 3.4e-08;				
Matches 128; Conservative 49; Mismatches 193; Indels 195; Gaps 30;				
Db	7	VILILSLFINQIKSANCPVGTETNTAGQVDLGLTPANCVNCO-----KNEY 52		Qy 7 VILILSLFINQIKSANCPVGTETNTAGQVDLGLTPANCVNCO-----KNEY 52
Db	1	MLLAIFYFVISTLPAKCTQTQTCCEAKCSEMYGTEICTRCQTGKVIDGKCYDATANAN 60		Db 1 MLLAIFYFVISTLPAKCTQTQTCCEAKCSEMYGTEICTRCQTGKVIDGKCYDATANAN 60
Qy	53	YNNAA-----AVPGATACTP-----CP-ORKDAGAQPNPATTANLVTOCNV 93		Qy 53 YNNAA-----AVPGATACTP-----CP-ORKDAGAQPNPATTANLVTOCNV 93
Db	61	CKNAGSGDGDANQVGKMMSSVPGNLQLCTTVSPDGCVSVANEEYFPVPPNADATHSDSVSCSE 120		Db 61 CKNAGSGDGDANQVGKMMSSVPGNLQLCTTVSPDGCVSVANEEYFPVPPNADATHSDSVSCSE 120
Qy	94	KCPACTA-----TAGAT-----DYAALITECVCRINFYNNENAPNFNAGASTC 137		Qy 94 KCPACTA-----TAGAT-----DYAALITECVCRINFYNNENAPNFNAGASTC 137
Db	121	ETPHLANKNQYIGVAGCATCSARKAQPAGEDNTPKAAATCKAAGFL--HTP--SEGJSC 176		Db 121 ETPHLANKNQYIGVAGCATCSARKAQPAGEDNTPKAAATCKAAGFL--HTP--SEGJSC 176
Qy	138	-TACPVNRYGGALTAGNAATIVACNVACPTGTLADDGVTTDVYRSFTECVKCRLNPFYNN 196		Qy 138 -TACPVNRYGGALTAGNAATIVACNVACPTGTLADDGVTTDVYRSFTECVKCRLNPFYNN 196
Db	177	EETPEGYFGHTATAESKRT----CK-SCTGGSS-----EAPNVKGIGDCLKC---MYN 222		Db 177 EETPEGYFGHTATAESKRT----CK-SCTGGSS-----EAPNVKGIGDCLKC---MYN 222
Qy	197	GNNGNTPFPNGKSCOTPCTCPAIPKPAVNAQATLGNDAT--ITAQCNVA-----CPDG ---		Qy 197 GNNGNTPFPNGKSCOTPCTCPAIPKPAVNAQATLGNDAT--ITAQCNVA-----CPDG ---
Db	223	EASNT-----LTCERKCSAQKPSL-DKTSCLNDCTGONCACFSGCGDSGFILD 275		Db 223 EASNT-----LTCERKCSAQKPSL-DKTSCLNDCTGONCACFSGCGDSGFILD 275
Qy	245	-----TISAAGVNNWAGNTCTCNPYNNNAPNFNPNFNGNSTCLCPANKDYG 294		Qy 245 -----TISAAGVNNWAGNTCTCNPYNNNAPNFNPNFNGNSTCLCPANKDYG 294
Db	276	GQNCKSDCKTENCKACTNPKAANEVCTE-----STHHLITPTSQCVOYCQALGRYYA 329		Db 276 GQNCKSDCKTENCKACTNPKAANEVCTE-----STHHLITPTSQCVOYCQALGRYYA 329
Qy	295	EATAGGAATLAKOCNIA----CPDGATASGATNNVYLQTECLNCAANFYFDGNINFOQAGS 350		Qy 295 EATAGGAATLAKOCNIA----CPDGATASGATNNVYLQTECLNCAANFYFDGNINFOQAGS 350
Db	330	GTNNDNKKKA-CKECTVANCKTND-----QGQOTCMBGFXKNGDACSPCH 374		Db 330 GTNNDNKKKA-CKECTVANCKTND-----QGQOTCMBGFXKNGDACSPCH 374
Qy	351	SRCKACPANKVQGAVATAGGTATLIAQCALECPAGTVL---TDGTTSTYKQ-----		Qy 351 SRCKACPANKVQGAVATAGGTATLIAQCALECPAGTVL---TDGTTSTYKQ-----
Db	375	ESCKTCSA-----GTA---SDCT-ECPTRGALKYGRNGTGCGEGCTTGQGSG 419		Db 375 ESCKTCSA-----GTA---SDCT-ECPTRGALKYGRNGTGCGEGCTTGQGSG 419
Qy	399	-----AASECVKC-----AANFYTTKQTDIVAGTIDCTCSC-----		Qy 399 -----AASECVKC-----AANFYTTKQTDIVAGTIDCTCSC-----
Db	420	ACRTCGLTIDGASYCSCEDTQNEYPQNGICITSTTAVTCKNSNYANGI---CSCTNGF 477		Db 420 ACRTCGLTIDGASYCSCEDTQNEYPQNGICITSTTAVTCKNSNYANGI---CSCTNGF 477
Qy	429	-----NKKLUTSGEAN 439		Qy 429 -----NKKLUTSGEAN 439
Db	478	LRMNNGCYETTKFPGKSVCEGANAD 502		Db 478 LRMNNGCYETTKFPGKSVCEGANAD 502
RESULT 6				
T42017				Cysteine rich protein - Giardia intestinalis
C;Species: Giardia intestinalis				C;Accession: T42017
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000				R;Chen, N.; Upcroft, J.
Parasitology 111, 423-431, 1995				#Title: A Giardia duodenalis gene
#Reference number: Z22027				#Accession: T42017
A;Accession: T42017				A;Status: preliminary; translated from GB/EMBL/DDJB

Sequence Comparison Results									
Query Match		Best Local Similarity		Score		Length			
		Pred.	No.	DB	2	DB	2	DB	2
Molecule type:	DNA								
Residues:	1-1274 <CHE>								
Cross-references:	EMBL:129079; NID:9951190; PID:9951191; PIDN:AAA74587.1								
Experimental source:	Homo sapiens								
Superfamily:	unassigned ankyrin repeat proteins								
Homology:	ankyrin repeat homology								
Y	Query Match	9.0%	Score: 228; DB 2; Length 1274;						
b	Best Local Similarity	23.1%	Pred. No. 2, 2e-07;						
b	Matches	119;	Conservative 35; Mismatches 183;						
b	Indels	178;	Gaps 30;						
b	21 ANCPV-GTENTNTAGQVDDLGTPANCYCNQKNFYNN-----NAAAFVPGASTCTPC 69								
b	801 APCRNVEGCETCVCVEGNAQ----NPPATANLYTQ-----CNVK-CPAGTAIAGGTDAVAILTEC 115								
b	70 PQKKDAGAQP----NPPATANLYTQ-----CNVK-CPAGTAIAGGTDAVAILTEC 115								
b	853 ---EGNAQOQCKTICRPGTINTDKQTCKDP-EAPCNVEGE-TCVESNA-----QQC 899								
b	116 VNCRINFYENAPNENAGPASTCTACPVNRYVGALLTAGNAATIVQAQCHYACPTGTALDGV 175								
b	900 KTCRPGY----TINTDKQTCKDP-----EAPCNV-----BGC 928								
b	176 TTDYVRSFSTECVKCRNLNFYNGNNG-----NTPPNPGKSQCTPOPAIKPANYVAQA 225								
b	929 ETVCVEGNAQOCKTICRPGTINTDKQTCKDP-EAPCNV-----NCKUCDNPTIDNET-C 981								
b	226 TLGNDATITACQNCVACPDEPIISAGV----NNVVAQNTECTNCAPNFVNNNAPNPNFGN 280								
b	982 TKCNGDGYLPTPNQCVPDCT-AISGGYGTDTKCKKACNECEACV-----GPAN 1029								
b	281 STCLCPANK--DYGAEAATAGGAATLAKCNCIA----OPD-----GRAIASATN--- 324								
b	1030 NCITACPVGKMLQYDFTDTNTPVNGTCMDQCSVSSTNDGGAECGAQIGGPAYCSCCKNTQQ 1089								
b	325 -----YVILOTECLINCAANFY-DG-----NNFOAGSSRC 353								
b	1090 APLNGNCASSRVAFCATTSGACTKCNQEYFLKGCGCTDROPGKQVCSNQGGNGKC 1149								
b	354 KACPANKVQGAVATAGGTATLIAQCALECPAGTVLTDGTGTTSTYKOAASECYKAANFYRT 413								
b	1150 QTC-----ANGLAASDGNC-AECHS---TCATCST-ADAADKCTCATGYKE 1192								
b	414 KQTDWYAGIDFTCSNCMRKLTSGAEEANLPESAKKNI 448								
b	1193 NGDDTAGL-CKKCSEKI-SGCKQCVSSGSSVI 1224								
RESULT	7								
Z25933	hypothetical protein W02C12.1 - Caenorhabditis elegans								
Z	Species:	Caenorhabditis elegans							
Z	Date:	15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999							
Z	Accession:	T25933							
Z	Description:	submitted to the EMBL Data Library, December 1996							
Z	Reference:	The sequence of C. elegans cosmid W02C12.							
Z	Accession:	Z20112							
Z	Status:	preliminary; translated from GB/EMBL/DDBJ							
Z	Source:	A. Molecular type: DNA							
Z	Residues:	1-1372 <MUR>							
Z	Cross-references:	EMBL:080815; PIDN:AAB37995_1; GSPDB:GN00022; CESP:W02C12.1							
Z	Experimental source:	strain Bristol N2; clone W02C12							
Z	Genetics:	C; Gene: CESP:W02C12.1							
Z	Introns:	A; Map position: 4							
Z	Gene:	C; Map position: 4							
Z	Accession:	C; Gene: CESP:W02C12.1							
Z	Position:	66/1: 774/2; 823/2; 1046/1; 1108/2; 1298/1							
Query Match	Match	8.6%	Score: 218.5; DB 2; Length 1372;						
Best Local Similarity	Similarity	22.2%	Pred. No. 9.7e-07;						
Matches	Conservative	35;	Mismatches 35;						
Gaps	Indels	125;	Gaps 125;						

Db	272	TSESA----ARAGTEETCTKCSNNLSPLGDACTLTDPCAGTYAVSGDGSVCKPCHNTC 327	Qy	387	VLTDCGTTSTYKQAASECVKCAANFY-----TTKQTDWAGIDTC 428
Qy	257	-----QINCTCNCAFNF---YNNNAPNPNPGNSTCL-----PCPANKDV 292	Db	439	-CPTNCASAKDNTKTCNCFSGSYLDTIAKACKCSETGGNIQGVENCSC 488
Db	328	AGCQTDDRETSCTACPGYSLLESNG----ATGRCVKEGTGAFITNCADGQCYAN---			
Qy	293	GAETATAAAATLAQCONIACPDG-----TAAISATATNYVILQT---ECLNCAANFY 340			RESULT 10
Db	380	-----VGG----AKYVQ-CQDGTAAGRDYVSCTATGGRCCTACTGNYAL 429			protocollaisin - sea urchin (<i>Strongylocentrotus purpuratus</i>) (fragment)
Qy	341	FDGNNFOA----GSSRKACPANKYQGAVAT-AGGTA----TIIAQACALECPAGTVLTD 390	C;Species:	Strongylocentrotus purpuratus (purple urchin)	
Db	430	LSGGCINTQTLPGSKYCKAV-ANSNDGKCKTCANCQAPDPATNFCPLCDSTCAESTKND 488	C;Date:	22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000	
Qy	391	GTTST----YKQAAASBCVKCAANFYTTCRDTWAGIDTGTSCNKLTS 435	C;Accession:	T30274	
Db	489	ADACTKCFPGYTKTGNCIRCTESSNNGKID--GIPDCLSCEAPINTG 535	R;Laidlaw, M.; Wessel, G.M.		
		A;Title: Cortical granule biogenesis is active throughout oogenesis in sea urchins.			
		A;Reference number: Z20803; MUID:94298531			
		A;Accession: T30274			
		A;Status: preliminary; translated from GB/EMBL/DDJB			
		A;Molecule type: mRNA			
		A;Residues: 1-1297 <LAD>			
		A;Cross-references: EMBL:U57753; NID:91373380; PID:91373379; PIDN:AAB02256.1			
		RESULT 9			
A48434	variant-specific surface protein - Giardia lamblia (strain GS/M)	Query Match 7.5%; Score 191.5; DB 2; Length 1297;			
C;Species:	Giardia lamblia	Best Local Similarity 21.2%; Pred. No. 5.1e-05;			
C;Date:	31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999	Matches 125; Conservative 63; Mismatches 192; Indels 211; Gaps 37;			
R;Nash, T.B.; Nowatt, M.R.					
Mol. Biochem. Parasitol. 51, 219-228, 1992					
A;Title: Characterization of a Giardia lamblia variant-specific surface protein (VSP) 96					
A;Reference number: A48434; MUID:92244292					
A;Accession: A48434					
A;Status: preliminary					
A;Molecule type: mRNA					
A;Residues: 1-557 <NAS>					
A;Cross-references: GB:M80480; NID:9159142; PID:9159143					
		Query Match 7.8%; Score 197; DB 2; Length 557;			
Best Local Similarity 20.7%; Pred. No. 1.1e-05;		Matches 110; Conservative 58; Mismatches 211; Indels 152; Gaps 25;			
Db	7	VILIISLFINQIKSANCPVGTETTAQVYDGLTPANCYVNCOKNHYNN----- 55			
Qy	1	MFLINCLIASTLAGCSTQANCYAERCMEVGETEICTQQNKYVPINGVCEAAASSNT .60			
Db	56	-----AAFPVGASTNTPC-----PKKKDAGA----- 77			
Qy	61	KCQKQSAADESDQCGKCLSLTFMYKGGYDKTKNLGRICKTPEFGSDAKGCAKNDKEGF 120			
Db	78	QPNPPATANLYTQCNVKC--PAGTAIAGGATDYAAITECVNCRINFNNENAPFNAGAS 135			
Db	121	FDNPDAA-ANVVDSC-ISCQDADTGTIPGSSTKTYKGVAAGCAK--TKPSQISENTGKREA 176			
Qy	136	TCTACPVNVRGGCATLGNATIVACNVA-CPTGTAALDDGVTIDYRSFTECVKCRLN 193			
Db	177	TCTCENANLYLKAVSSPTSAT--SCVSAEDCKGYF---PTDTDTDSKKCLTC--- 225			
Qy	194	YYNGNGNTPPNPGQSQTCPATKPAQAT-----GNDATTAQCNVACPGT 245			
Db	226	-----STADKGIDGCSACELIPSSTRASITYLISCSACSTNNSPLKNECMQDCPAGT 278			
Qy	246	ISAAGV-----NNWYAQNTE-CTNCAP---NFTNNNAAPNF-----NPGN 280			
Db	279	YADSVCKCPANKDGYGEATAG----GAAFLAKQCNIACPDGTIAASGATNYVILQTECLNC 338			
Qy	281	STCLCPCPANKDGYGEATAG----GAAFLAKQCNIACPDGTIAASGATNYVILQTECLNC 335			
Db	339	GQCATIAGSKYKCRCKSGFVNVGLCVAETARAAPPGST---PDKTNGV---CTAC 390			
Qy	336	ANWFYDF-GNNFQA---GSSRKACP-----VQGAVATAGGTTIAQALECPAGT 386			
Db	391	TEKFLESGGCYQAEKFRGNTLCTTADAGKCTTCANGQDKDSNGS-----CPA- 438			
		RESULT 11			
		T22759			
		hypothetical protein F55H12.3 - Caenorhabditis elegans			
		C;Species: Caenorhabditis elegans			
		C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Aug-2000			
		C;Accession: T22759			

A;Experimental source: clone H10524
 R;McMurray, A.
 Submitted to the EMBL Data Library, October 1996

A;Reference number: 219610
 A;Accession: T22759
 A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA
 A;Residues: 1-2824 <WIL>
 A;Cross-references: EMBL:281091; PIDN:CA03143.1; GSPDB:GN00019; CESP:F55H12.3
 A;Experimental source: clone F55H12
 C;Genetics:
 A;Gene: CESP:F55H12.3
 A;Map position: 1 98/1; 126/2; 201/3; 343/3; 406/1; 576/3; 656/1; 825/3; 869/1; 909/1; 96/1; 1755/2; 1800/1; 1850/3; 2035/3; 2082/3; 2113/1; 2144/1; 2200/2; 227/1; 2433-279/Domain: LDL receptor ligand-binding repeat homology <LDL>

Query Match Score 190.5; DB 2; Length 2824;
 Best Local Similarity 21.9%; Pred. No. 0.00012;
 Matches 117; Conservative 42; Mismatches 207; Indels 169; Gaps 25;

Qy 20 SANCPVGTT-----NTAGQVDDLGTPANCYNNQKNNYNNAAAFVEGASTCTPCQQKKD 74
 Db 2123 SVKQFGROAKANNYNSTSCDKRLLPTVLRQPKNLRKGTTEDFT----- 2168

Qy 75 AGAQNPNPATANLYTQCNVKCPAGTAINGATDYAALITECYNCRNFNEYENAPNPNAGA 134
 Db 2169 -----KVEMP-----DEDDVAFFDNIVGIRTEVNYHNGQQFGVGI 2202

Qy 135 STCTACPVNRGGATTAGNAATIVQCNV-----ACPT-----GTALDDGVITDVRSFSTE 185
 Db 2203 FTV-----RYVGDAGNSAECTFDVTYQKOSQVYAEGTVALAMOFTTAPETKAE 2256

Qy 186 CVKCRUNFY-----YNGNNENTP-----YNGNNENTP-----YNGNNENTP----- 2314
 Db 2257 KVQCDDNLYPTDSRPMFYQCDIMSDYQIGWSDNTKQIYLPAGQTS-----PAVQAINGTV 2314

Qy 225 ATLGNDATI-----TAQCN-----VACP-----DGTAAG-----VNNWVQANTEC 261
 Db 2315 VSGCQQQIHLQRDVIWASADCDELSCLRMIVPSCDFIDGRYVIADELSNTALQYTF 2374

Qy 262 TNCA-----PNFVNNAAPNF-----MNGNSTCLCPANKDGYGAETAGGAATLAQCNIA 312
 Db 2375 TKNATETIDTVLHQTNNTYIROSDFYCDP-----SYPHDHGTVNIVCKV-----C 2424

Qy 313 PDGTAIASGANYVILQTCUANAFYFDGNNFQAGSSRKACPANKYGOVAYATAGSTA 372
 Db 2425 PEGT-----PANKESN-----KCIDCPINTYRNSTNL-----OLKCTRACTGTTVYGDYTGAVDE 2474

Qy 373 TLIAOCALECPAGTVLTDG-----TTSTYK-----QAASECVKCAANFY 411
 Db 2475 ---SQCVNCVPICPGQFSEKGLNCPCEGFTGPTGLRKC1CCGFEDLISTFGGPCLQOPRGLT 2531

RESULT 13
 T43291

C;Species: Caenorhabditis elegans
 C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
 C;Accession: T43291
 C;Status: preliminary; translated from GB/EMBL/DDBJ

R;Zhu, X.; Kao, G.; Joh, K.; Hall, D.H.; Wadsworth, V.K.; Hutter, H.; Vogel, B.E.; Hu R;Barlow, K.
 A;Reference number: Z19669
 A;Accession: T23064
 A;Status: preliminary; translated from GB/EMBL/DDBJ

C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
 C;Accession: T23064; T25096
 R;Barlow, K.
 A;Reference number: Z19669
 A;Accession: T23064
 A;Molecule type: DNA
 A;Residues: 1-2823 <WIL>
 A;Cross-references: EMBL:AF074902; PIDN: AAC26793.1
 C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like
 C;Genetics:
 A;Map position: 1
 A;Map position: 1-2
 A;Note: laminin alpha-1
 C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like

Query Match Similarity 7.4%; Score 188.5; DB 2; Length 3102;
 Best Local Similarity 21.5%; Pred. No. 0.00018; Mismatches 32; Indels 160; Gaps 30;

Qy 22 NCPVGETNTA-----GVDLIG-----TP 41
 Db 860 NGCPLGEVNKECYCSDFGGFPPLTKCIECTCNCNIDPQIGNQDSETOKCLKIGHFTG 919

Qy 42 ANCVCNQKPNYNNAAAFVPGASTCPCPKKKDAQAQPNNPATANLYTQC---NVKCPAG 98
 Db 920 DSCESC-KEHHWNAQ---LHKCKPGCHTQQAVNP-----OCSEEEGECBK 963

Qy 99 TAIAGGATDYAAITTECVNRINFYNNENAPNENAGASTCTACPVNRYVGALTANARIV 158
 Db 964 ENYIG-----AQCDREK----ENHGDVENG---CPACDNDTG5---IGSDCDQVS 1004

Qy 159 AQCNVACPTGTALDDGVTIDYVR---SETE---CVKCRUNFYNGNNGNTPFNNGKSQC- 211
 Db 1005 GQCN-----CKOGYF---GKOCDQCRPSXENFDAGQFCHNIVGIEDGKCDQ7GKCSR 1059

Qy 212 ---TPCPAIKP-----IVVADA---TLGNDAT-----TVAQCNVACPDTGTTSAAGV 251
 Db 1060 ENVESTMCMERCADGYFVNITSGGCGEDCGDPGSVEDVSCNLVTCQC-VCKPG-----1110

Qy 252 NWVAQNTECTCNAFPNNNNAPNPNGSTCLCPANKDYGATAAGGAATLAKQCNIA 311
 Db 1111 ---VGLKDSCLPNFYGT----SEGCPCECP-----APQVCDPTDGCSV 1152

Qy 312 CPDGTAIASATGATNNVYLQTECLNCNAANF-YFDGNNFQGSSRKCACPANKVQGAVATAG 369
 Db 1153 CPPNT-----VGENCCTNNAWHDYHPNG-----CKLCDCSD---IGSDG 1190

Qy 370 GTA-TIIQACALECPAGTVLTDGTSTYKQIASSBCVKCAANFTTKQIDDWVAGIDTCPSC 428
 Db 1191 GMCTNETGQC---KCKAAAYV-----GLKCDLCTHGF-----NPTCEPC 1227

RESULT 14

Laminin gamma-1 chain precursor - human
 C; Species: Homo sapiens (man)
 C; Date: 30-Jun-1991 #sequence-revision 30-Jun-1991 #text_change 10-Dec-1999
 R; Kallunki, T.; Ikonen, J.; Chow, L.T.; Kallunki, P.; Tryggvason, K.
 J. Biol. Chem. 266, 221-228, 1991
 A; Title: Structure of the human laminin B2 chain gene reveals extensive divergence from
 R; Pikkariainen, T.; Kallunki, T.; Tryggvason, K.
 A; Status: nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 1-1609 <KAL>
 A; Reference number: A28158; MUID:08198245

A; Molecule type: mRNA
 A; Cross-references: EMBL:J03202; NID:9186916; PID:AAA59488.1; PID:9307107
 R; Fukushima, Y.; Pikkariainen, T.; Kallunki, T.; Eddy, R.L.; Byers, M.G.; Haley, L.L.; He
 Cytoogenet. Cell. Genet. 48, 137-141, 1988
 A; Title: Isolation of a human laminin B2 (LAMB2) cDNA clone and assignment of the gene t
 R; Pikkariainen, T.; Kallunki, T.; Tryggvason, K.
 A; Accession: S13548; MUID:89169663

A; Molecule type: mRNA
 A; Cross-references: EMBL:1333-1609 <FKUK>

A; Cross-references: EMBL:M27654; NID:9186923; PID:AAA59489.1; PID:9186924

R; Olsen, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,

Lab. Invest. 60, 772-782, 1989
 A; Title: Human laminin: Cloning and sequence analysis of cDNAs encoding A, B1 and B2

A; Reference number: A34961; MUID:89280632

A; Accession: B34961

A; Molecule type: mRNA

A; Residues: 868-151; 'N', 1553-1609 <OLS>

R; Santos, C. L. S.; Sabbaga, J.; Brentani, R.

DNA Seq. 1, 275-277, 1991

A; Title: Differences in human laminin B2 sequences

A; Reference number: S14664; MUID:92216129

A; Accession: S14664

A; Molecule type: mRNA

A; Residues: 1282-1609 <SAN>

A; Cross-references: EMBL:X13939; NID:934237; PID:CAA32122.1; PID:g34238

R; Viollete, R.; Kallunki, T.; Chow, L.; Pikkariainen, T.; Tryggvason, K.

in Extracellular Matrix Genes, Sandell, L.J. and Boyd C.D., eds., pp. 175-193, Academi

A; Title: Genes for the human laminin B1 and B2 chains.

A; Reference number: S25566

A; Accession: S25566

A; Molecule type: DNA

A; Residues: 801-1481; 'R', 1483-1609 <VVOO>

A; Note: mRNA was also sequenced

C; Genetics:

A; Gene: GDB:LAMC1; LAMB2

A; Cross-references: GDB:120136; OMIM:150290

A; Map position: 1q31-1q31

A; Introns: 140/1, 241/3; 285/2; 341/1; 404/1; 443/2; 476/2; 522/1; 563/1; 626/2; 664/

C; Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin

C; Function:

A; Description: Interact with cells and with other basement membrane proteins to promote

C; Superfamily: laminin beta-1 chain; laminin-type EGF-like homology

C; Keywords: basement membrane; laminin binding; coiled coil; extracellular

F; 1-33//Domain: signal sequence #status predicted <SGC>

F; 34-1609//Product: laminin gamma-1 chain #status predicted <WAT>

F; 34-285//Domain: VI #DOM6>

F; 286-504//Domain: V #DOM5>

F; 286-339//Domain: laminin-type EGF-like homology <LE01>

F; 342-395//Domain: laminin-type EGF-like homology <LE02>

F; 398-442//Domain: laminin-type EGF-like homology <LE03>

F; 445-492//Domain: laminin-type EGF-like homology <LE04>

F; 495-504//Domain: laminin-type EGF-like homology #status atypical <LE05>

F; 505-659//Domain: IV #DOM4>

F; 690-721//Domain: laminin-type EGF-like homology #status atypical <LE02>

F; 724-770//Domain: laminin-type EGF-like homology <LE07>

F; 773-825//Domain: laminin-type EGF-like homology <LE08>

F; 828-881//Domain: laminin-type EGF-like homology <LE09>

F; 884-932//Domain: laminin-type EGF-like homology <LE10>

F; 935-980//Domain: laminin-type EGF-like homology <LE11>

F; 983-1028//Domain: laminin-type EGF-like homology <LE12>

F; 1035-1609//Domain: II/I <DOM1>

F; 1035-1609//Region: heptad repeats

F; 40-50//Disulfide bonds: #status Predicted

F; 10-134,576,650-1022,1107,1161,1175,1205,1223,1241,1380,1395,1439//Binding site: carb

F; 1031,1034,1600//Disulfide bonds: interchain #status Predicted

Query Match Similarity 7.4%; Score 188; DB 1; Length 1609;

Best Local Similarity 23.9%; Pred. No. 0.00011; Matches 99; Conservative 28; Mismatches 165; Indels 122; Gaps 26;

Qy 75 AGAOPNPATANLVTCNVKCPAGTAGATAGGTDYAA1ITECVNCRINFYNEAPNPNFNGA 134

Db 674 ASARPGPGVPAWVEST--CPVG--YGGF-----CEMC-LSGYRRETGP-Y 718

A; Title: Isolation of a human laminin B2 (LAMB2) cDNA clone and assignment of the gene t

R; Pikkariainen, T.; Kallunki, T.; Tryggvason, K.

A; Accession: A28158

A; Molecule type: mRNA

A; Cross-references: EMBL:J03202; NID:9186916; PID:AAA59488.1; PID:9307107

R; Fukushima, Y.; Pikkariainen, T.; Kallunki, T.; Eddy, R.L.; Byers, M.G.; Haley, L.L.; He

Cytoogenet. Cell. Genet. 48, 137-141, 1988

A; Title: Isolation of a human laminin B2 (LAMB2) cDNA clone and assignment of the gene t

R; Pikkariainen, T.; Kallunki, T.; Tryggvason, K.

A; Accession: S13549

A; Molecule type: mRNA

A; Cross-references: EMBL:1333-1609 <FKUK>

A; Cross-references: EMBL:M27654; NID:9186923; PID:AAA59489.1; PID:9186924

R; Olsen, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,

Db 758 YYGDSTAGTS-----SDCQPCPGSSCAVVPKTKEVCTNCPTGTTGK-----RCE 805

RESULT 15

T42215
 Zonadhesin - mouse
 N;Alternate names: sperm-specific membrane protein
 C;Species: Mus musculus (house mouse)
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C;Accession: T42215
 R;Gao, Z.; Garbers, D.L.
 J. Biol. Chem. 273, 3415-3421, 1998
 A;Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane protein
 A;Reference number: 98123114
 A;Accession: T42215
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-5376 <GAO>
 A;Cross-references : EMBL:U97068; NID:93327421; PIDN: AAC26680.1
 C;Genetics:
 A;Gene: Zan
 A;Map position: 5
 C;Function:
 A;Description: functions in multiple cell adhesion processes
 A;Note: found exclusively on the apical region of the sperm head
 C;Keywords: cell adhesion

Query Match 7.4%; Score 188; DB 2; Length 5376;
 Best Local Similarity 21.2%; Pred. No. 0.00031;
 Matches 114; Conservative 52; Mismatches 184; Indels 188; Gaps 30;

Qy 17 QIKSANCPVGTETNTAGQYDLDGPANCVN----CQKHFYNNAAAVPGASTCTP-C-- 69
 Db 3151 QCQNQCPPLKTYCK----DLKDGSNTNIPLOQCPNSRVTNC----LSPCPPLCLD 3199

Qy 70 PQKKRAGAQINPPATANLYTQCNV----COPAGATAAGGGTIDAYAIIITECVNCINF 122
 Db 3200 PEGLCGTSKPKVPSKCREGCICOPGGYLMHKRNKC----VLRIFCGOKNTOGAF 3247

Qy 123 YNENPNNAGASTOCTACPVNRVGALTAGNAATIVAQC-NYACPTGFALDDGVTDYVR 181

Db 3248 ISADTWISRGCTQSTCPC----AGAI-----HCRNFCKPSGT----- 3281

Qy 182 SFTEVCRUNFYNGNNGNTPN----PGKSQCTPC-----PAIKP 219

Db 3282 -----YCKNNDGSSNCTEITLQCPNTNSQFTDCLPSVPSCSNRCEVTPSPV-P 3329

Qy 220 ANVAATLGNDIAT-----TAQCNYACPDGTTSAAGVNNWVA-----NTE 260

Db 3330 SSRCBSCLCHHGFWVISEDKCPVPRTCQGCKDARGAIPIAG-KWITSKGCTQSACACVEGNIQ 3388

Qy 261 CTN---CAPNFYNNNNPNNPFGNSTC----LPCPANKDGAEEATA-----GAAATLA 305

Db 3389 CQNFQCPPEY---TKDNSSGSSTKTILQCPAHHTQ7ISCLPSCLDPGLCKGASPRVPSKEGCCCTQSGYVLSNPKCLL 3445

Qy 306 KQCNIACPDGTAIASGATNNVILQTECLCAANFYFDGNNFQAGSSRCKACPANKVQGAV 365

